

# *Nppc* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Nppc*

**Project type**

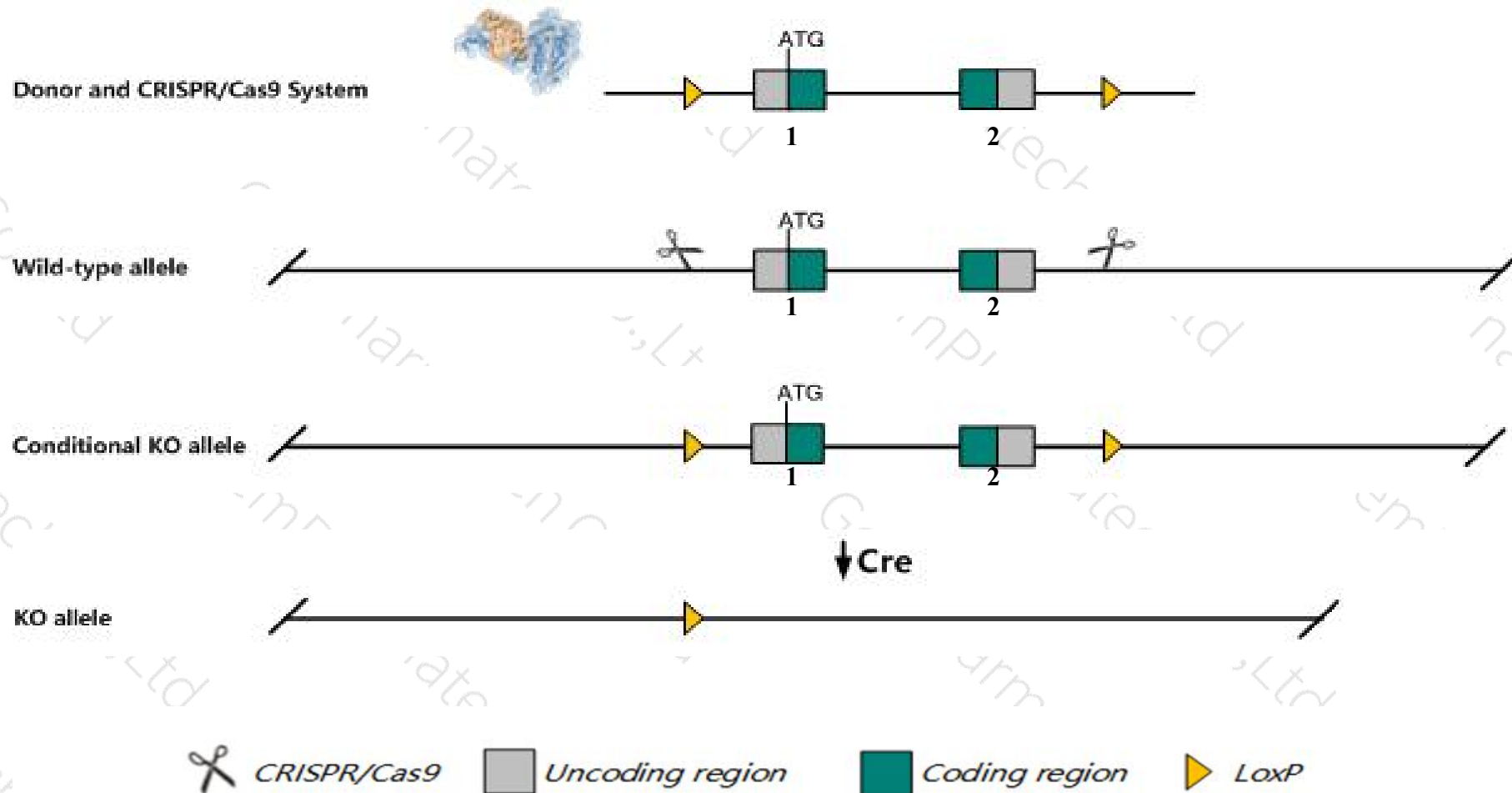
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nppc* gene. The schematic diagram is as follows:



- The *Nppc* gene has 1 transcript. According to the structure of *Nppc* gene, exon1-exon2 of *Nppc-201* (ENSMUST00000027449.5) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nppc* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, homozygotes for a targeted null mutation exhibit severe dwarfism due to impaired endochondral ossification. Mutants are viable at birth, but fewer than half survive postnatal development. Mice homozygous for a knock-out allele exhibit abnormal secondary sensory axon bifurcation.
- The *Nppc* gene is located on the Chr1. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.



# Gene information (NCBI)

## Nppc natriuretic peptide type C [ *Mus musculus* (house mouse) ]

Gene ID: 18159, updated on 1-Oct-2019

### Summary

Official Symbol	Nppc provided by MGI
Official Full Name	natriuretic peptide type C provided by MGI
Primary source	MGI:MGI:97369
See related	<a href="#">Ensembl:ENSMUSG00000026241</a>
Gene type	protein coding
RefSeq status	REVIEWED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CNP; Ibab
Summary	This gene encodes a member of the natriuretic peptide family. Natriuretic peptides are involved in the control of blood pressure, extracellular fluid volume and electrolyte homeostasis. The encoded protein also plays a role in sensory neuron bifurcation, and is a critical regulator of endochondral bone growth. The encoded protein is a ligand for the natriuretic peptide receptor B, and is synthesized as a prohormone which is cleaved to produce a mature peptide. Mutations in this gene are associated with dwarfism resulting from impaired endochondral ossification. [provided by RefSeq, Apr 2011]
Expression	Biased expression in ovary adult (RPKM 20.5), cerebellum adult (RPKM 4.7) and 7 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

### Genomic context

Location: 1 C5; 1 43.98 cM

See Nppc in [Genome Data Viewer](#)

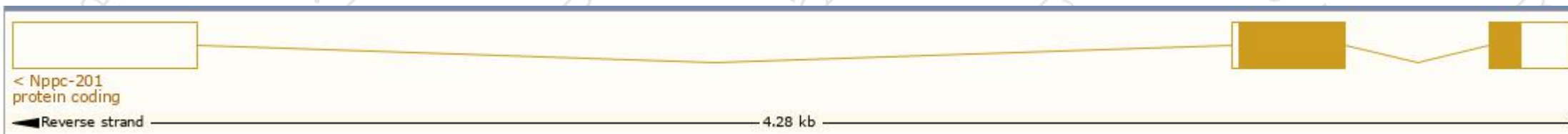
Exon count: 3

# Transcript information (Ensembl)

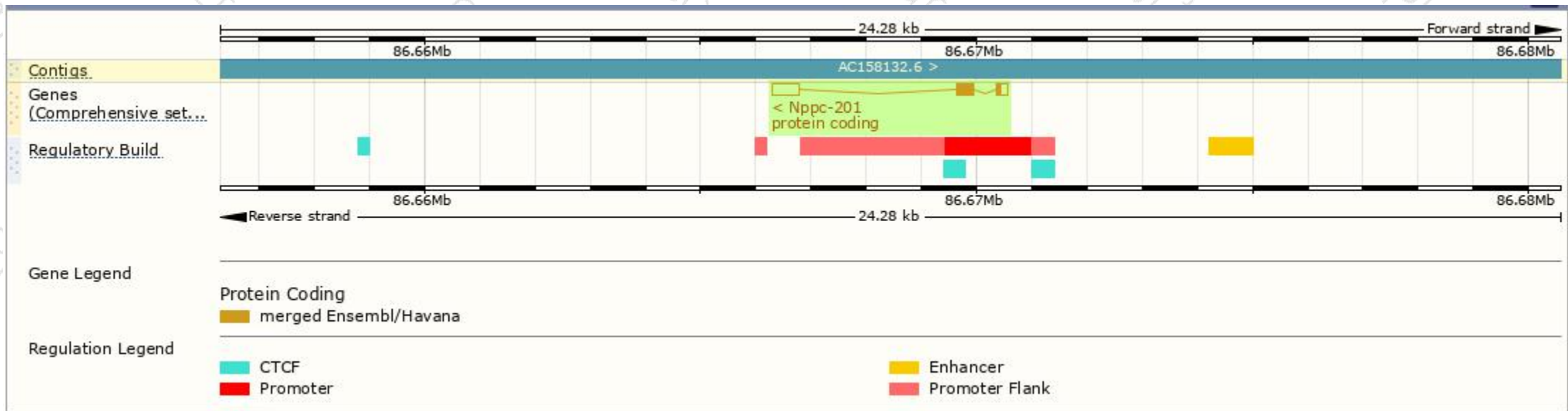
The gene has 1 transcript, the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nppc-201	<a href="#">ENSMUST00000027449.5</a>	1042	<a href="#">126aa</a>	Protein coding	<a href="#">CCDS15123</a>	<a href="#">Q544K5</a> <a href="#">Q61839</a>	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Nppc-201* transcript, The transcription is shown below

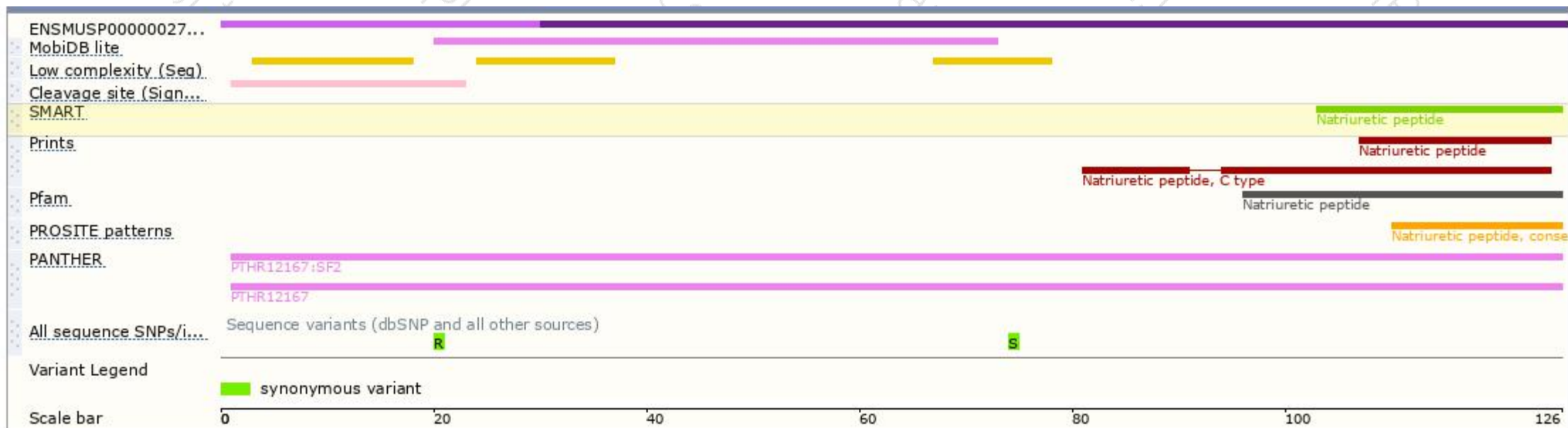


# Genomic location distribution



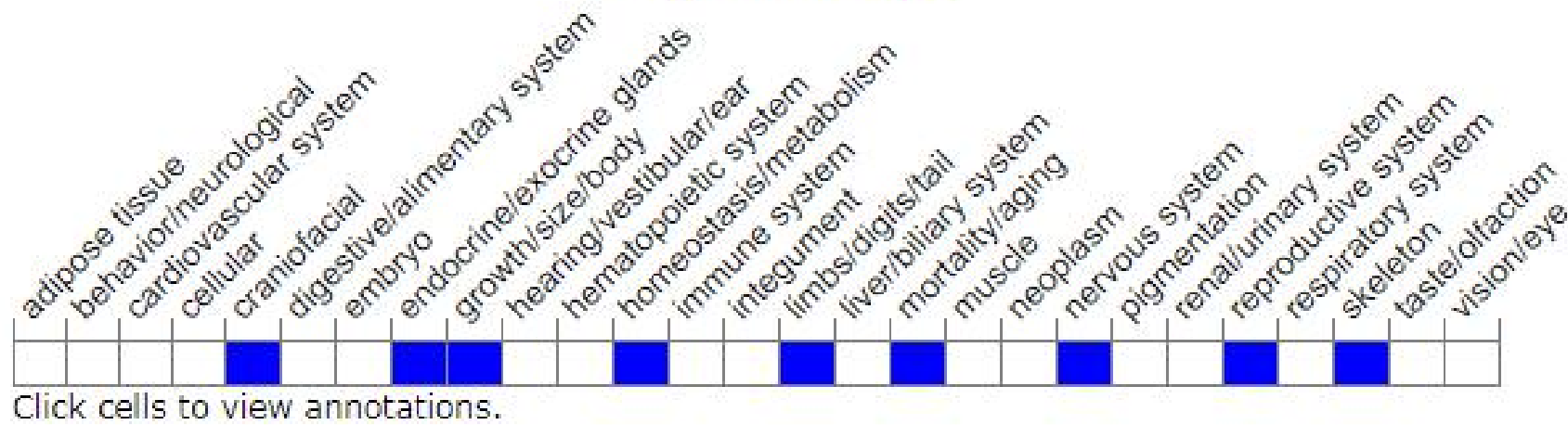


# Protein domain



# Mouse phenotype description(MGI)

## Phenotype Overview ?



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

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If you have any questions, you are welcome to inquire.

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